

SEQUENCE LISTING

<110> University of Utah Research Foundation
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<120> Omega-Conopeptides

<130> 2314-241

<150> US 09/910,082
 <151> 2001-07-23

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 <151> 2001-02-05

<160> 413

<170> PatentIn version 3.0

<210> 1
 <211> 318
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<220>
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 aatttctcca cgttgactcg tcgctgcctt tctcccgat cacgatgtca taagacaatg 180
 cgtaactgct gcacttcatg ctcttcatac aaagggaaat gtcggcctcg aaaatgaacc 240
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 caaaaaaaaa aaaaaaaaaa 318

<210> 2
 <211> 76
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 2
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 1 5 10 15

2

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu
 35 40 45
 Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser
 50 55 60
 Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
 65 70 75

<210> 3
 <211> 30
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue
 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 3
 Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
 1 5 10 15
 Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys
 20 25 30

<210> 4
 <211> 283
 <212> DNA
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 4
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 ctcatcacag ctgatgactc cagaggtacg cagaagcatc atgccctgag gtcgaccacc 120
 aatttctcca cgctcgactcg tcgctgcaaa cctcccggaa gaaaatgtct gaatagaaaag 180
 aatgaatgct gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa 240
 aactgaataa aagccgcatt gcaaaaaaaaa aaaaaaaaaa aaa 283

<210> 5
 <211> 74
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 5
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 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys
35 40 45

Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys Ser Lys
50 55 60

Phe Cys Asn Glu His Leu His Met Cys Gly
65 70

<210> 6
<211> 27
<212> PRT
<213> Unknown

<220>
<223> unknown Conus species

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu;
Xaa at residue 3 and 4 is Pro or Hyp

<400> 6
Cys Lys Xaa Xaa Gly Arg Lys Cys Leu Asn Arg Lys Asn Xaa Cys Cys
1 5 10 15

Ser Lys Phe Cys Asn Xaa His Leu His Met Cys
20 25

<210> 7
<211> 275
<212> DNA
<213> Unknown

<220>
<223> unknown Conus species

<400> 7
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aatctctcca tatcgtctcg ctgcaaacct cccagaagaa aatgtctgaa gattaaggat 180
aaatgctgca actttttgcaa tacacaccta aatatgtgtg gataaatggc taaaaactga 240
ataaaagccg cattgcaaaa aaaaaaaaaa aaaaa 275

<210> 8
<211> 72
<212> PRT
<213> Unknown

<220>
<223> unknown Conus species

<400> 8
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro
 35 40 45
 Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys
 50 55 60
 Asn Thr His Leu Asn Met Cys Gly
 65 70

<210> 9
 <211> 26
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<220>
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 <223> Xaa at residue 3 and 4 is Pro or Hyp

<400> 9
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 1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys
 20 25

<210> 10
 <211> 377
 <212> DNA
 <213> Unknown

<220>
 <223> unknown Conus species

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 aaactctcca tgtcgactcg ctgcgcaggt ccaggaacaa tttgtcctaa taggggatgc 180
 tgcgggttatt gcagtaaaag aacacatcta tgtcattcgc gaactggctg atcttccccc 240
 ttctgcgctc catccttttc tgcctgagtc ctccatacct gagaatggtc atgaaccact 300
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 aaaaaaaaaa aaaaaaa 377

<210> 11
 <211> 74
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 11

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Met Ala
 1 5 10 15
 Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly
 35 40 45
 Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
 50 55 60
 Arg Thr His Leu Cys His Ser Arg Thr Gly
 65 70

<210> 12
 <211> 28
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at
 residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 12
 Cys Ala Gly Xaa Gly Thr Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
 20 25

<210> 13
 <211> 323
 <212> DNA
 <213> Conus arenatus

<400> 13
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 ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120
 actaggcagt gctcggctaa cggtggatct tgtactcgtc attttcactg ctgcagcctc 180
 tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300
 caataaaaaa aaaaaaaaaa aaa 323

<210> 14
 <211> 73
 <212> PRT
 <213> Conus arenatus

<400> 14
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
 35 40 45
 Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
 50 55 60
 Ser Val Cys Val Ala Thr Ser Tyr Pro
 65 70

<210> 15
 <211> 33
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 15
 Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 16
 <211> 326
 <212> DNA
 <213> Conus arenatus

<400> 16
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 ctgagggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat 180
 tgtactttgc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcatgttca 240
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 ctgcattgaa ataaaagccg cattgc 326

<210> 17
 <211> 74
 <212> PRT
 <213> Conus arenatus

<400> 17
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
 20 25 30

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<210> 18
<211> 28
<212> PRT
<213> Conus arenatus
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<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa
      at residue 5 is Pro or Hyp; Xaa at residue 8 and 19
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
      O-sulpho-Tyr or O-phospho-Tyr

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<400> 18
Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys
1          5          10          15

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Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
20 25

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<210> 19
<211> 332
<212> DNA
<213> Conus arenatus
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ctgagggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cgggtggatct 180
tgtttctcgtc atttttactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240
gcaacctcat acccgtgagt ggtcatgaac cactcaatac cctctcctct ggaggcttca 300
gaggaactgc attgaaataa aagccgcatt gc 332
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<210> 20
<211> 79
<212> PRT
<213> Conus arenatus
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<400> 20
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1          5          10          15
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Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
35 40 45

Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
50 55 60

Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro
65 70 75

<210> 21
<211> 33
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(33)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
4 and 33 is Pro or Hyp; Xaa at residue 19 and 32 is
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 21
Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15
Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa
20 25 30

Xaa

<210> 22
<211> 332
<212> DNA
<213> Conus arenatus

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gacaaaaact ccaagttgac caggacatgc aacactccca ccgaatattg tactttgcat 180
caacactgct gcagcggcta ctgccataaa acaatccagg catgttcata ataccggtga 240
gtggatcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
aaaaccgcat tacaaaaaaa aaaaaaaaaa aa 332

<210> 23
<211> 74
<212> PRT
<213> Conus arenatus

<400> 23
Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
20 25 30
His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
35 40 45
Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
50 55 60
Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
65 70

<210> 24

<211> 28
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa
 at residue 5 is Pro or Hyp; Xaa at residue 8 and 19
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 24
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
 20 25

<210> 25
 <211> 394
 <212> DNA
 <213> Conus arenatus

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 gacaaaaact cccagttgac cagggaaatgc acacctcccg gtggagcttg tggtttacct 180
 acacactgct gcggggttttg cgatactgca aacaacagat gtctgttaaag ctggtctggc 240
 gtctgatatt ccccttctgt gctctatcct ctttgacctg agtcatecgt acctgtgagt 300
 ggtcatgaac tactcaatac cctctcctct ggaggcttca gaggaactac aatgaaataa 360
 aaccgcatt gcagagaaaa aaaaaaaaaa aaaa 394

<210> 26
 <211> 73
 <212> PRT
 <213> Conus arenatus

<400> 26
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 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
 20 25 30
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
 35 40 45
 Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
 50 55 60
 Cys Asp Thr Ala Asn Asn Arg Cys Leu
 65 70

<210> 27
 <211> 27
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 5 and 12 is Pro or Hyp

<400> 27
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 1 5 10 15
 Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
 20 25

<210> 28
 <211> 345
 <212> DNA
 <213> Conus arenatus

<220>
 <221> misc_feature
 <222> (1)..(345)
 <223> n may be any nucldeotide

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 ctcattacag ctgagactta ctccagaggt gagcagaatc accatgttct gaggtcaact 120
 gacaaaaact ccaagttgac caggacatgc aacactccca ctgaatattg tactttgcat 180
 caacactgct gcagcggcca ctgccataaa acaatccagg catgtgcata ataccggtgg 240
 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
 aaaaccgcat tgcaatgaan aaaaaaaaaa aaaaaaaaaa aaaaa 345

<210> 29
 <211> 74
 <212> PRT
 <213> Conus arenatus

<400> 29
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His
 20 25 30
 His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45
 Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
 50 55 60
 His Cys His Lys Thr Ile Gln Ala Cys Ala
 65 70

<210> 30
 <211> 28
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(28)

<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 30

Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys
1 5 10 15

Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
20 25

<210> 31

<211> 322

<212> DNA

<213> Conus arenatus

<400> 31

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actaggcagt gctcgccctat cggatggatat tgtactcttc atattcactg ctgcagcaac      180
cattgcatta aacctatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggatcatgaac      240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg      300
caataaaaaa aaaaaaaaaa aa                                           322

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<210> 32

<211> 70

<212> PRT

<213> Conus arenatus

<400> 32

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr
35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile
50 55 60

Gly Arg Cys Val Ala Thr
65 70

<210> 33

<211> 30

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 33

Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
 1 5 10 15

Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr
 20 25 30

<210> 34
 <211> 318
 <212> DNA
 <213> Conus arenatus

<400> 34
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 ctactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120
 actaggcagt gcttgcctaa cgggtggatat tgtactcttc atattcactg ctgcagcgac 180
 cattgcatta aacctatcga ccgatgtgtg gcaacctgat acccgggcgt ggtcatgaac 240
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300
 caaaaaaaaa aaaaaaaaaa 318

<210> 35
 <211> 70
 <212> PRT
 <213> Conus arenatus

<400> 35
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr
 35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile
 50 55 60

Asp Arg Cys Val Ala Thr
 65 70

<210> 36
 <211> 30
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 4 and 23 is Pro or Hyp; Xaa at residue 8 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 36
 Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
 1 5 10 15

Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr
 20 25 30

<210> 37
 <211> 374
 <212> DNA
 <213> Conus aurisiacus

<400> 37
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 tccatgtcga ctgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc 180
 tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgac ttcccccttc 240
 tgtgtcttat ccttttctgc ctgagtcctc cttacctgag agtggtcatg aaccactcat 300
 cacctgctcc tctggaggcc ccagaggagc tacattgaaa taaaagtcgc attgcaaaaa 360
 aaaaaaaaaa aaaa 374

<210> 38
 <211> 71
 <212> PRT
 <213> Conus aurisiacus

<400> 38
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser
 50 55 60
 Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 39
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 39
 Cys Lys Gly Lys Gly Lys Xaa Cys Ser Arg Ile Ser Xaa Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 40
 <211> 380
 <212> DNA
 <213> Conus aurisiacus

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<400> 40
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tccatgtcga ctggctgcat ggaagccgga tcttattgcg gctctactac gagaatctgc      180
tgcggttttt gcgcttattt cggcaaaaaa tgtattgact atcccagcaa ctgatcttcc      240
ccctactgtg ctctatcctt ttctgcctga gtctctctta cctgagagtg gtcatgaacc      300
actcatcacc tgctcctctg gagggcccag aggagctaca ttgaaataaa atcgcatctgc      360
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<210> 41
<211> 77
<212> PRT
<213> Conus aurisiacus

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<400> 41
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu
          35          40          45
Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys
          50          55          60
Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
65          70          75

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<210> 42
<211> 32
<212> PRT
<213> Conus aurisiacus

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<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa
      at residue 30 is Pro or Hyp; Xaa at residue 7, 21
      and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
      di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 42
Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys
1          5          10          15
Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn
          20          25          30

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<210> 43
<211> 373
<212> DNA
<213> Conus aurisiacus

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<400> 43
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg      60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttcctg      120

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agctcggcca ccaaactctc catgtcgact cgctgcaagg ctaaaggaaa accatgcagt      180
aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgtg ctgatccagt      240
gcctgatctt cccctttctg tgetctatcc ttttctgcct gagtcctcct tacctgagag      300
tggtcatgaa ccactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata      360
aaagccgcat tgc                                                         373

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<210> 44
<211> 71
<212> PRT
<213> Conus aurisiacus

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<400> 44
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
          35          40          45
Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
          50          55          60
Cys Arg Ser Gly Lys Cys Gly
65          70

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<210> 45
<211> 25
<212> PRT
<213> Conus aurisiacus

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<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
      O-sulpho-Tyr or O-phospho-Ty

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```

<400> 45
Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
1          5          10          15
Thr Gly Ser Cys Arg Ser Gly Lys Cys
          20          25

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<210> 46
<211> 379
<212> DNA
<213> Conus aurisiacus
<400> 46

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accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg      60
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg      120
aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt      180
ggatttgaca acgactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg      240
atccagegcc tgatcttccc ctttctgtgc tctatccttt tctgcccagag tcctccttac      300

```

ctgagagtgg tcatgaacca ctcatcacct gctccctgga ggcctcagag gagctacaat 360
gaaataaaag cgcgattgc 379

<210> 47
<211> 72
<212> PRT
<213> Conus aurisiacus

<400> 47
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
20 25 30
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
35 40 45
Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
50 55 60
Asp Pro Gly Arg Asn Ile Cys Thr
65 70

<210> 48
<211> 26
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 48
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15
Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr
20 25

<210> 49
<211> 382
<212> DNA
<213> Conus bullatus

<400> 49
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120
aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgcgga 180
cctgctacta cgaaaatctg ctgcgatttt tgcagtcctat tcagcgatag atgtatgaac 240
aatcccaaca attgatcttc ccccttgtgt gctccatcct tttctgctg agtcctcctt 300
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360
attgaaataa aagccgcatt gc 382
<210> 50

<211> 78
 <212> PRT
 <213> Conus bullatus

<400> 50
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45
 Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
 50 55 60
 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
 65 70 75

<210> 51
 <211> 36
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa
 at residue 13, 25 and 34 is Pro or Hyp; Xaa at
 residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 51
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30
 Asn Xaa Asn Asn
 35

<210> 52
 <211> 400
 <212> DNA
 <213> Conus bullatus

<400> 52
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaacaccc tgtgtcgact cgctgcatta ctccaggaac acgatgtaa 180
 gttccgagcc aatgctgcag aggtccttgc aagaacggtc gttgtactcc atccccttct 240
 gaatggtaaa tgtggttgat ccagcgctg atcttcccc ttcgtcgtgc tccatccttt 300
 tctgcctgag tctcctttac ctgagagtgg tcatgaacca ctcatcacct actcccctgg 360
 aggcttcaga ggagctacat tgaaataaaa gccgcattgc 400

<210> 53
 <211> 76

<212> PRT

<213> Conus bullatus

<400> 53

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys His Pro Val Ser Thr Arg Cys Ile Thr
 35 40 45

Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Gly Pro Cys
 50 55 60

Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
 65 70 75

<210> 54

<211> 31

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 11, 18, 26 and 28 is Pro or Hyp; Xaa
 at residue 31 is Trp or Bromo-Trp

<400> 54

Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg
 1 5 10 15

Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa
 20 25 30

<210> 55

<211> 379

<212> DNA

<213> Conus bullatus

<400> 55

accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt 180
 ggtattcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgtagctg 240
 atccggcgctc ttgatactcc gcttctgtgc tccatctttt ctgcctgagt cctccttacc 300
 tgagagtggc catgaaccac tcatcaccta ctctcttgga ggcttttagag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 56

<211> 72

<212> PRT

<213> Conus bullatus

<400> 56

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys
 50 55 60
 Asp Pro Ala Arg Arg Thr Cys Thr
 65 70

<210> 57
 <211> 26
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 57
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr
 20 25

<210> 58
 <211> 373
 <212> DNA
 <213> Conus bullatus

<400> 58
 accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 180
 aggattgcgt ataactgctg caagtattct tgcagaaatg gtaaagtgtg ctgatccagc 240
 gcctgatctt ccccttctgtg tgetccatcc ttttctgcct gagtcctcct tacctgagag 300
 tggatcatgaa ccaactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360
 aaagccgcat tgc 373

<210> 59
 <211> 71
 <212> PRT
 <213> Conus bullatus

<400> 59
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
 35 40 45

Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
 50 55 60

Cys Arg Asn Gly Lys Cys Gly
 65 70

<210> 60
 <211> 25
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13
 and 18 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 60
 Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Lys Xaa Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 61
 <211> 382
 <212> DNA
 <213> Conus bullatus

<400> 61
 atcaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120
 aagtcgacct ccaaagtctc caagtcgact agctgcatgg cagccggatc ttattgcgga 180
 cctgctacta cgaatatctg ctgcgatttt tgcagtccat tcagcgatag atgtatgaaa 240
 aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt 300
 acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360
 attgaaataa aagccgcatt gc 382

<210> 62
 <211> 78
 <212> PRT
 <213> Conus bullatus

<400> 62
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala
 35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe
50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn
65 70 75

<210> 63
<211> 36
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at
residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 63
Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys
20 25 30

Lys Xaa Asn Asn
35

<210> 64
<211> 373
<212> DNA
<213> Conus bullatus

<400> 64
accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc agctcattat agctgaggac tccagaggta cgcagttgca tcgtgccctg 120
aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180
aggacttcgt atgactgctg cacgggttct tgcagaaatg gtagatgtgg ctgatccagc 240
gcctgatctt ccccttctg tgetccatcc ttttctgcct gagtcctcct tacctgagag 300
tggtcatgaa ccaactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360
aaagccgcat tgc 373

<210> 65
<211> 71
<212> PRT
<213> Conus bullatus

<400> 65
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
35 40 45

Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
50 55 60

Cys Arg Asn Gly Arg Cys Gly
65 70

<210> 66
<211> 25
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 66
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys
20 25

<210> 67
<211> 321
<212> DNA
<213> Conus characteristicus

<400> 67
ggatccatga aactgacgtg cgtgggtgatc atcgccgtgc tgttcctgac ggccctgtcaa 60
ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120
actaggcagt gctcggctaa cggtggatct tgtactcgtc attttctactg ctgcagcctc 180
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300
caaaaaaaaaa a 321

<210> 68
<211> 73
<212> PRT
<213> Conus characteristicus

<400> 68
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
50 55 60

Ser Val Cys Val Ala Thr Ser Tyr Pro
65 70

<210> 69
<211> 33
<212> PRT
<213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 69
 Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 70
 <211> 26
 <212> PRT
 <213> Conus catus

<400> 70
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly
 20 25

<210> 71
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 71
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Arg Cys
 20 25

<210> 72
 <211> 229
 <212> DNA
 <213> Conus catus

<400> 72
 tcgactcgct gccagggtag aggagcatca tgctgtaaga ctatgtataa ctgctgcagc 60
 gggttcttgca acagaggtag ttgtggctga tccggcgct gatcttcccc cttccgtgct 120
 ctatcctttt ctgcctgatt cctccttacc tgagagcggt catgaaccac tcatcacctg 180
 ctctcttgga ggcctcagag gagctacatt gaaataaaag ccgcattgc 229

<210> 73
 <211> 29

<212> PRT
 <213> Conus catus

<400> 73
 Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr
 1 5 10 15
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly
 20 25

<210> 74
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 74
 Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Asn Arg Gly Ser Cys
 20 25

<210> 75
 <211> 235
 <212> DNA
 <213> Conus catus

<400> 75
 tcgacacgct gcttgccctgc cggagagtct tgccttttta gtaggattag atgctgcggt 60
 acttgacggt cagtcttaaa gtcattgtgt agctgatcca gctgctgac ttctctctcc 120
 tgtgtccat ccttttctgc ctgagtcctc cttatctgag agtggtcatg aaccactcac 180
 cacctactct tctggaggct tcagaggagc tacagtgaat taaaagccgc attgc 235

<210> 76
 <211> 31
 <212> PRT
 <213> Conus catus

<400> 76
 Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile
 1 5 10 15
 Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
 20 25 30

<210> 77
 <211> 28
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa
 at residue 3 is Pro or Hyp

<400> 77
 Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
 20 25

<210> 78
 <211> 227
 <212> DNA
 <213> Conus catus

<400> 78
 tcgacacgct gccagggtag aggaggacca tgtactaagg ctgtgtttta ctgctgcagc 60
 gggtcttgca acagaggtag atgtggctga tccagcgcct gatcttcccc cttctgtgct 120
 ctatcctttt ctgcctgagt cctccttact gagagtagtc atgaaccact catcacctac 180
 tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc 227

<210> 79
 <211> 29
 <212> PRT
 <213> Conus catus

<400> 79
 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
 20 25

<210> 80
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp

<400> 80
 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 81
 <211> 236
 <212> DNA
 <213> Conus catus

<400> 81
 ttaactttgc gctgcgcaac ttacggaaaa ctttgtggtta ttcaaaacga ctgctgcaat 60
 acatgcgata cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccctt 120
 ctgtgctcta tccttttctg cctgagtcct cttacctga gagtgggtcat gaaccactca 180
 tcacctgctc ctctggaggc ctcgggggag ctacattgaa ataaaagccg cattgc 236

<210> 82

<211> 30
 <212> PRT
 <213> Conus catus

<400> 82
 Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn
 1 5 10 15
 Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25 30

<210> 83
 <211> 26
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 83
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 84
 <211> 229
 <212> DNA
 <213> Conus catus

<400> 84
 tcgactcgct gccggggttag aggaggacca tgtactaagg ctatgttttaa ctgctgcagc 60
 ggttcttgca acagaggttag atgtggctga tccagcgct gatcttcccc cttctgtgct 120
 ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta 180
 ctcctctgga ggcctcagag aagcatcatt gaaataaaag ccgcattgc 229

<210> 85
 <211> 29
 <212> PRT
 <213> Conus catus

<400> 85
 Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe
 1 5 10 15
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
 20 25

<210> 86
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp

<400> 86

Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 87

<211> 374

<212> DNA

<213> Conus circumcisis

<400> 87

acaaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180
 aagactatgt ataactgctg cagcggttct tgcagcaacg gtagatgtgg ctgatccagc 240
 gcctgatctt ccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga 300
 gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360
 aaaagccgca ttgc 374

<210> 88

<211> 71

<212> PRT

<213> Conus circumcisis

<400> 88

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser
 50 55 60

Cys Ser Asn Gly Arg Cys Gly
 65 70

<210> 89

<211> 25

<212> PRT

<213> Conus circumcisis

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 89

Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys
 20 25

<210> 90
 <211> 379
 <212> DNA
 <213> Conus circumcisis

<400> 90
 accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggcca ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgccgc 180
 tctactacga gaacctgctg cggttattgc tcttatttca gcaaaaaatg tattgacttt 240
 cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctgagt cctccttacc 300
 tgagagtggg catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 91
 <211> 77
 <212> PRT
 <213> Conus circumcisis

<400> 91
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45
 Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60
 Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn
 65 70 75

<210> 92
 <211> 35
 <212> PRT
 <213> Conus circumcisis

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
 residue 33 is Pro or Hyp; Xaa at residue 10, 21 and
 24 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 92
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe
 20 25 30
 Xaa Ser Asn
 35

<210> 93
 <211> 379
 <212> DNA
 <213> Conus circumcisis

<400> 93
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcggaca ccaaactccc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180
 aggcttatgt atgactgctg cagcggttct tgcagcaggt actcaggtag atgtggctga 240
 tccagcgcct gatcttcccc cttctgctgc tctatccttt tctgcctgag tcttccttac 300
 ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggcccagag gagctacatt 360
 gaaataaaag ccgcattgc 379

<210> 94
 <211> 73
 <212> PRT
 <213> Conus circumcisis

<400> 94
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser
 35 40 45
 Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60
 Cys Ser Arg Tyr Ser Gly Arg Cys Gly
 65 70

<210> 95
 <211> 27
 <212> PRT
 <213> Conus circumcisis

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 95
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys
 20 25

<210> 96
 <211> 379
 <212> DNA
 <213> Conus circumcisis

<400> 96
 accaaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120
 acgtcggcca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc 180
 tctactacga gaacttgctg cggttattgc gcttatttcg gcaaaaaatg tattgactat 240
 cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctaagt cctccttacc 300
 tgagagtggg catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 97
 <211> 77
 <212> PRT
 <213> Conus circumcisis

<400> 97
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys
 35 40 45
 Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60
 Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
 65 70 75

<210> 98
 <211> 35
 <212> PRT
 <213> Conus circumcisis

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 98
 Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
 20 25 30
 Xaa Ser Asn
 35

<210> 99
 <211> 362
 <212> DNA
 <213> Conus consors

<400> 99
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60

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acagctgatg actccagagg tacgcagaag catcgtgccc tgaagtctta caccaaactc 120
tccatgttaa ctttgcgctg cgcattcttac ggaaaacctt gtggtattga caacgactgc 180
tgcaatacat gcgatccagc cagaaagaca tgtacgtagc tgatccggcg tctgatcttc 240
ccccttctgt gctctatcct tttctgcctg agtcctcctt acctgagagt ggtcatgaac 300
cactcatcac ctagctcctc tggaggcttc agaggagcta caatgaaata aaagcgcatt 360
gc 362

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<210> 100
<211> 72
<212> PRT
<213> Conus consors

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<400> 100
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
          35          40          45
Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys
          50          55          60
Asp Pro Ala Arg Lys Thr Cys Thr
65          70

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<210> 101
<211> 26
<212> PRT
<213> Conus consors

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<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
      residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
      di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 101
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
1          5          10          15
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
          20          25

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<210> 102
<211> 237
<212> DNA
<213> Conus consors

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<400> 102
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120
tccatgtcga ctgctgcaa gggtagagga aaaccatgca gtaggattgc gtataactgc 180

```

tgacaccgggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgac tcccccc 237

<210> 103
 <211> 71
 <212> PRT
 <213> Conus consors

<400> 103
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60
 Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 104
 <211> 25
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 104
 Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 105
 <211> 320
 <212> DNA
 <213> Conus consors

<400> 105
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60
 acagctgatg actccaaagg tacgcagaag catcggtccc tgaggctgac caccaaagtc 120
 tccaaggcga ctgactgcat tgaagccgga aattattgcy gacctactgt tatgaaaatc 180
 tgctgcggct tttgcagtcc atacagcaaa atatgtatga actatcccca aaattgatct 240
 tcccccttct gtgetctatc cttttctgcc tgagtcctcc ttacctgaga gtgggtcatga 300
 accactcatc acctcgcccc 320

<210> 106
 <211> 78
 <212> PRT
 <213> Conus consors

<400> 106

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
 35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
 50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn
 65 70 75

<210> 107

<211> 36

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
 residue 13, 25 and 34 is Pro or Hyp; Xaa at residue
 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 107

Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
 20 25 30

Xaa Xaa Gln Asn
 35

<210> 108

<211> 321

<212> DNA

<213> Conus consors

<400> 108

atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60

acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120

tccatgtcga ctcgctgcaa aggtaaaagga gcatcatgta caaggcttat gtatgactgc 180

tgccacgggt cttgcagcag cagcaagggt agatgtggct gatccggcgc ctgatcttcc 240

cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagaggt ggtcatgaac 300

cactcatcac ctgctcccct g 321

<210> 109

<211> 73

<212> PRT

<213> Conus consors

<400> 109

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser
 50 55 60
 Cys Ser Ser Ser Lys Gly Arg Cys Gly
 65 70

<210> 110
 <211> 27
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 110
 Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
 20 25

<210> 111
 <211> 292
 <212> DNA
 <213> Conus consors

<400> 111
 ggatccatga aactgacgtg catggtgacg gtcgccgtgc tgctcctgac ggccctgtcaa 60
 ctcacacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120
 aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180
 gactgctgca ccggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240
 cccttctgtg ctctatcctt ttctgcctga gtcattcata cctgtgctcg ag 292

<210> 112
 <211> 71
 <212> PRT
 <213> Conus consors

<400> 112
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Lys Cys Gly
 65 70

<210> 113
 <211> 25
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 113
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 114
 <211> 299
 <212> DNA
 <213> Conus consors

<400> 114
 ggatccatga aactgacgtg cgtggtgata gtcgccgtgc tgctcctgac ggccctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgaa gtcggacacc 120
 aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac 180
 gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240
 atcttccccc ttctgtgctc tacccttttc tgcctgagtc atccatacct gtgctcgag 299

<210> 115
 <211> 72
 <212> PRT
 <213> Conus consors

<400> 115
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
 50 55 60
 Asp Pro Ala Arg Lys Thr Cys Thr
 65 70

<210> 116
 <211> 26
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at

residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 116

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
20 25

<210> 117

<211> 434

<212> DNA

<213> Conus consors

<220>

<221> misc_feature

<222> (1)..(434)

<223> n may be any nucleotide

<400> 117

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ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggccctgtcaa      60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc      120
aaactctcca tgtcgactcg ctgcaagggt acaggaaaac catgcagtag ggttgcgatat      180
aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc      240
cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc      300
actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg      360
cantgnanaa aannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnggaaaaaaa      420
aaaaaaaaaa aaaa                                     434

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<210> 118

<211> 71

<212> PRT

<213> Conus consors

<400> 118

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
50 55 60

Cys Arg Ser Gly Lys Cys Gly
65 70

<210> 119

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 119

Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 120

<211> 393

<212> DNA

<213> Conus consors

<400> 120

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ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggctgtgcaa      60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc      120
aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attgccgctc tactacgaga      180
acctgctgcg gttattgcgc ttatttcggc aaattttgta ttgactttcc cagcaactga      240
tcttccccct actgtgctct atccttttct gcctctgcct gagtcctcct tacctgagag      300
tggtcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata      360
aaagccgcat tgcaaaaaaaaa aaaaaaaaaa aaa                                393
```

<210> 121

<211> 77

<212> PRT

<213> Conus consors

<400> 121

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn
65 70 75

<210> 122

<211> 35

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
21 and 24 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 122
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe
 20 25 30

Xaa Ser Asn
 35

<210> 123
 <211> 361
 <212> DNA
 <213> Conus dalli

<400> 123
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg 120
 aggtcgacca tcaaacactc catgttgact aggagctgca cgctccccgg aggaccttgt 180
 gggtattata atgactgctg cagtcatcaa tgcaatataa gcagaaataa atgcgagtag 240
 ctgatccggc atctgatctt ccccttctgt gctcgtccta acctgagagt ggtcatgaac 300
 catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360
 c 361

<210> 124
 <211> 73
 <212> PRT
 <213> Conus dalli

<400> 124
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr
 35 40 45

Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
 50 55 60

Cys Asn Ile Ser Arg Asn Lys Cys Glu
 65 70

<210> 125
 <211> 28
 <212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 5 and 8 is Pro or Hyp; Xaa at residue
 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 125

Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa
 20 25

<210> 126
 <211> 350
 <212> DNA
 <213> Conus distans

<400> 126
 accaaaacca tcataaaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcctg 60
 acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa 120
 acctccgggt caacgaagag atgcgaagat cctggtgaac cttgcggaag tgatcattcc 180
 tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctggtctgg catctgacca 240
 ttcccccttct gtactctatc tctattgcct gagtcatctt tacctgtgag tggatcatgaa 300
 tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350

<210> 127
 <211> 66
 <212> PRT
 <213> Conus distans

<400> 127
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser
 20 25 30

Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro
 35 40 45

Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val
 50 55 60

Cys Ala
 65

<210> 128
 <211> 25
 <212> PRT
 <213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu;
 Xaa at residue 4 and 7 is Pro or Hyp

<400> 128
 Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
 1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
 20 25

<210> 129
 <211> 309
 <212> DNA

<213> Conus ermineus

<400> 129

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atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc      60
acagctgacg actccagacg tacgcagaag catcgtgccc tgaggtcgac caccaaacgc      120
gccacgtcga atcgcccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac      180
tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta      240
tccttttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc      300
ctctggagg                                     309
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<210> 130

<211> 72

<212> PRT

<213> Conus ermineus

<400> 130

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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
          20          25          30
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
          35          40          45
Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys
          50          55          60
Thr Cys Thr Arg Ser Lys Cys Pro
65          70
```

<210> 131

<211> 27

<212> PRT

<213> Conus ermineus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1, 4, 11 and 27 is Pro or Hyp

<400> 131

```
Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1          5          10          15
Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa
          20          25
```

<210> 132

<211> 308

<212> DNA

<213> Conus ermineus

<400> 132

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aactcatcac agctgatgac tccagaggta cgcagaacga tcgtgccctg aggtcgacca      60
ccaaactctc catgctgact cgggcctgct ggtcttccgg aacaccttgt ggtactgata      120
gtttatgctg cggtggatgc aatgtatcca aaagtaaag taactagctg attcggcgctc      180
```


tgaacttccc ccttctgtgc tctatccttt tctgcccagag tcctccatac ctgagaatgg 240
 tcatgaacca ctcacacact actcctctgg agacctcaga agagctacac tgaaataaaa 300
 gcgcttgc 308

<210> 133
 <211> 54
 <212> PRT
 <213> Conus ermineus

<400> 133
 Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu
 1 5 10 15
 Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser
 20 25 30
 Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val
 35 40 45

Ser Lys Ser Lys Cys Asn
 50

<210> 134
 <211> 27
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is
 Trp or Bromo-Trp

<400> 134
 Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 135
 <211> 385
 <212> DNA
 <213> Conus geographus

<400> 135
 ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggccctgtcaa 60
 ctcacacag ctgatgactc cagaggtacg cagaagcacc gtgccttggg gtcgaccacc 120
 gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180
 aattgctgca ggtcttgcaa tccatacgcc aaaagatgtt acggctaata cagcgccctga 240
 tcttccccct tctgtgtctt atcccttctt gtctgagtcc tccttacctg agagtgggtca 300
 tgaaccactc ctcacactact tctctggagg cttcggagga gctacattga aataaaagcc 360
 gcattgtaaa aaaaaaaaaa aaaaa 385

<210> 136
 <211> 73
 <212> PRT

<213> Conus geographus

<400> 136

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
50 55 60

Asn Pro Tyr Ala Lys Arg Cys Tyr Gly
65 70

<210> 137

<211> 27

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
residue 13, 22 and 27 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr

<400> 137

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa
20 25

<210> 138

<211> 396

<212> DNA

<213> Conus geographus

<400> 138

ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa	60
ctcatcacag ctgatgactc cagaggtagc cagaagcatc gtgccctgag gtcgtccacc	120
aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt	180
gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgctacta acccagcgcc	240
tgatcttccc ccttctgtgc tctattcctt tctgcctgag tctctcttac ctgaaagtgg	300
tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa	360
gccgcattgc aatgacaaaa aaaaaaaaaa aaaaaa	396

<210> 139

<211> 74

<212> PRT

<213> Conus geographus

<400> 139

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 35 40 45
 Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys
 50 55 60
 Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
 65 70

<210> 140
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at
 residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 140
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15
 Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
 20 25

<210> 141
 <211> 407
 <212> DNA
 <213> Conus geographus

<400> 141
 ggaattccgt ttctgcgctg cttccttttg catcaccaaa accatcatca aaatgaaact 60
 gacgtgtgtg gtgatcgtcg ccgtgctgct cctgacggcc tgtcaactca tcacagctga 120
 tgactccaga ggtacgcaga agcatcgtgc cctggggctcg accaccgaac tctccttgtc 180
 gactcgtgc aagtcacccg gatcttcatg ttcaccgact agttataatt gctgcaggtc 240
 ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg 300
 agtcctcctt acctgagagt ggatcatgaac cactcatcac ctacttctct aggcgggttcg 360
 gaggagctac attgaaataa aagccgcatt gcaaaaaaaaa aaaaaaa 407

<210> 142
 <211> 73
 <212> PRT
 <213> Conus geographus

<400> 142
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 50 55 60

Asn Pro Tyr Thr Lys Arg Cys Tyr Gly
 65 70

<210> 143
 <211> 27
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13, 22 and 27 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 143
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa
 20 25

<210> 144
 <211> 28
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13, 22 and 27 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 144
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly
 20 25

<210> 145
 <211> 26
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 145
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys
20 25

<210> 146
<211> 314
<212> DNA
<213> Conus geographus

<400> 146
catcacagct gatgactcca gaggtacgca gaagcatcgt gccctgaggt cgtccaccaa 60
actcaccttg tcgactcgct gcaaatacacc cggaactcca tgttcaaggg gtatgcgtga 120
ttgctgcacg tcttgcttgt tatacagcaa caaatgtagg cgctactaac ccagcgcctg 180
atcttcccc ttctgtgctc tattcctttc tgcttgagtc ctccttacct gaaagtggtc 240
atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc 300
cgcatigcaa tgac 314

<210> 147
<211> 55
<212> PRT
<213> Conus geographus

<400> 147
Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg
1 5 10 15
Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr
20 25 30
Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr
35 40 45
Ser Asn Lys Cys Arg Arg Tyr
50 55

<210> 148
<211> 29
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 148
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
1 5 10 15
Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
20 25

<210> 149
<211> 29
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 149

Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
1 5 10 15

Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa
20 25

<210> 150

<211> 380

<212> DNA

<213> Conus laterculatus

<400> 150

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac cgctgatgac tccagaggtg cgcagaagca tcgtgccctg 120
aggtcgacca ccaatctctc catgctgact cggaagtgtc ggccttcctg aagctattgt 180
cgtgcgaata gtaaagtctg cagtggatgc gatcggaaca gaaataaatg ttactagctg 240
attcggcgtc tgaacttctc ccttctgtgc tctatccttt tctgcccagag tctccatac 300
ctgagagtgg tcatgaacca ctcaactcct actcctctgg aggcctcaga agagctacat 360
tgaaataaaa gccgcattgc 380

<210> 151

<211> 72

<212> PRT

<213> Conus laterculatus

<400> 151

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
35 40 45

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
50 55 60

Asp Arg Asn Arg Asn Lys Cys Tyr
65 70

<210> 152

<211> 27

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo-Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 152

Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa
 20 25

<210> 153

<211> 367

<212> DNA

<213> *Conus laterculatus*

<400> 153

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaaactctc catatcgact cgctgccttc ctcccggatc atattgtaag 180
 gcgacaacgg aagtctgctg ctcttcttgc cttcaattcg ctcagatatg ttcggggtga 240
 tcttcctct tctgtgctct atccttttct gcctgagtc tccatacctg agaatggtca 300
 tgaaccactc aacatctact cctctggagg cctcagaaga gctatattga aataaaagcc 360
 gcattgc 367

<210> 154

<211> 73

<212> PRT

<213> *Conus laterculatus*

<400> 154

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro
 35 40 45

Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys
 50 55 60

Leu Gln Phe Ala Gln Ile Cys Ser Gly
 65 70

<210> 155

<211> 27

<212> PRT

<213> *Conus laterculatus*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa
 at residue 3 and 4 is Pro or Hyp; Xaa at residue 7
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 155

Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys
 1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
20 25

<210> 156
<211> 373
<212> DNA
<213> Conus laterculatus

<400> 156
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccggatc atcatgtagc 180
gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240
ggctgaactt ccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300
tggtcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360
aaagccgcat tgc 373

<210> 157
<211> 75
<212> PRT
<213> Conus laterculatus

<400> 157
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
35 40 45
Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys
50 55 60
Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly
65 70 75

<210> 158
<211> 29
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residue 3 is Pro or Hyp

<400> 158
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
1 5 10 15
Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
20 25

<210> 159
<211> 330
<212> DNA
<213> Conus laterculatus

<400> 159
 accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacaa ccaaactctc catgctgact cggacctgct ggccttccgg aacagcttgt 180
 ggtattgata gtaactgctg cagtggatgc aatgtatcca gaagtaaagtg taactagctg 240
 attcggcgctc taaacttcct ccttctgcct gagtccctcca tacctgagag tggatcatgaa 300
 ccacatcatc acctcatctc tggaggcctc 330

<210> 160
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 160
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp
 35 40 45
 Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys
 50 55 60
 Asn Val Ser Arg Ser Lys Cys Asn
 65 70

<210> 161
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp

<400> 161
 Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
 1 5 10 15
 Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
 20 25

<210> 162
 <211> 363
 <212> DNA
 <213> Conus laterculatus

<400> 162
 accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaatctctc catgctgact cggaagtgtc ggccttccgg aagctattgt 180

cgtgcgaata gtaaattgctg cagtggatgc gatcggaaca gaagtaaattg taactagctg 240
 attcggcgctc taaacttctc cctttctgcct gagtcctcca tacctgagag tggatcatgaa 300
 ccactcatca cctactctctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360
 tgc 363

<210> 163
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 163
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45
 Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
 50 55 60
 Asp Arg Asn Arg Ser Lys Cys Asn
 65 70

<210> 164
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is
 Trp or Bromo-Trp; Xaa at residue 8 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 164
 Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15
 Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 165
 <211> 391
 <212> DNA
 <213> Conus leopardus

<220>
 <221> misc_feature
 <222> (1)..(391)
 <223> n may be any nucleotide

<400> 165
 atgaaactga cgtgtgtggt gatcgtagct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaag cgctcgtgctc tgaggtcgac caccaaactc 120
 tccaggtcgc tctttgagtg cgcgccttcc ggtggacgtt gtgggttttt aaagtcctgc 180

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tgccaaggat attgcgatgg ggaaagcact tcatgtgtga gtggcccata cagcatctga 240
tcttcccgcc ttcagtgtc tacccttttc tgccctgagtc ctccatacct ctgagcggtc 300
atgaaccact caacacctac tcctctggag gcttcagga actatattaa aataaagccg 360
cattgcaacg aaanaaaaaa aaaaaaaaaa a 391

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<210> 166
<211> 79
<212> PRT
<213> Conus leopardus

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<400> 166
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg
          20          25          30
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala
          35          40          45
Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr
          50          55          60
Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile
65          70          75

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<210> 167
<211> 37
<212> PRT
<213> Conus leopardus

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<220>
<221> PEPTIDE
<222> (1)..(37)
<223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy
      Glu; Xaa at residue 7 and 34 is Pro or Hyp; Xaa at
      residue 22 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr,
      di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 167
Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys
1          5          10          15
Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser
          20          25          30
Gly Xaa Xaa Ser Ile
          35

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<210> 168
<211> 365
<212> DNA
<213> Conus leopardus

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<400> 168
atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60
acagctgaca tctccagagg tacgtggaag catcggtgtg tggggtcgac caccggactc 120
tccccgtggc ccttggaactg cacggctccc agtcaacctt gtggttattt tcttaggtgc 180

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tgtggacatt gcgatgtacg cagggatatgt acgagtggct gatccggcgt ctgatctttc 240
 cgccttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggtcatgaac 300
 cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg 360
 caatg 365

<210> 169
 <211> 73
 <212> PRT
 <213> Conus leopardus

<400> 169
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg
 20 25 30
 Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr
 35 40 45
 Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys
 50 55 60
 Asp Val Arg Arg Val Cys Thr Ser Gly
 65 70

<210> 170
 <211> 30
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa
 at residue 1 is Trp or Bromo-Trp; Xaa at residue 14
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 170
 Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa
 1 5 10 15
 Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 171
 <211> 381
 <212> DNA
 <213> Conus leopardus

<400> 171
 atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaag catcgtgctc tgaggctgac caccaaactc 120
 tccaggtcgc cctctaggtg catgtctccc ggtggaattt gtggtgattt tggtgactgc 180
 tgcgaaattt gcaatgtgta cggtatatgt gtgagtgact tacccggcatt ctgatctttc 240
 cgccttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac 300

cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg 360
 caaaaaaaaa aaaaaaaaaa a 381

<210> 172
 <211> 77
 <212> PRT
 <213> Conus leopardus

<400> 172
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met
 35 40 45
 Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys
 50 55 60
 Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 65 70 75

<210> 173
 <211> 31
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 and 29 is Pro or Hyp; Xaa at residue
 21 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 173
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa
 1 5 10 15
 Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile
 20 25 30

<210> 174
 <211> 404
 <212> DNA
 <213> Conus leopardus

<400> 174
 atgaaactga cgtgtgtggt gatcgctcgt gtgctgttcc tgacggcctg tcaactcact 60
 acagctgatg attccagagg tacacggaag catcgtgctc tgaggccaac caccaaactc 120
 tccaggtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc 180
 tgcggatatt gcgaaacggt ttacaatacg ttagatgag ttggctgac cggcgcttga 240
 tctttccgcc ttctgttgc ctatcttttt ctgcctgagt cctcccatac cccgttgagt 300
 ggtccatgaa ccaactccaac acctactccc tccttgaag cttccaaagg aaacgacatt 360
 taaaataaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 404

<210> 175
 <211> 72
 <212> PRT
 <213> Conus leopardus

<400> 175
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala
 35 40 45
 Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys
 50 55 60
 Glu Thr Phe Tyr Asn Thr Cys Arg
 65 70

<210> 176
 <211> 27
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 and 5 is Pro or Hyp; Xaa at residue 1,
 18 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 5 10 15
 Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg
 20 25

<210> 177
 <211> 292
 <212> DNA
 <213> Conus lynceus

<400> 177
 atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60
 acagctgatg actccagacg tacacagaag catcggtgcc tgaggctgac caccaatctc 120
 tccatgtcga ctgctgcaa gtctcccgga tcacatgta gtgtgacatc gtataactgc 180
 tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac 240
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg 292

<210> 178
 <211> 75
 <212> PRT
 <213> Conus lynceus

<400> 178
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
35 40 45

Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys
50 55 60

Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
65 70 75

<210> 179

<211> 30

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 179

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys
1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu
20 25 30

<210> 180

<211> 355

<212> DNA

<213> Conus lynceus

<400> 180

atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60

acagctgatg actccagagg tacgcagaag catcgctgcc tgaggctcgac caccaaacta 120

tccatgtata ctgctgctgc aggtccagga gcaatttgct ctaatagggt atgctgctgt 180

tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc ccccttctgt 240

gctctatcct ttttctgctt gctcctcca tacctgagaa tggatcatgaa ccaactcatca 300

cctactcctc ttggagacct cagaggagct aactgaaat aaaagccgca ttggc 355

<210> 181

<211> 74

<212> PRT

<213> Conus lynceus

<400> 181

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly
35 40 45

Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly
 65 70

<210> 182
 <211> 28
 <212> PRT
 <213> Conus lynceus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at
 residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 182
 Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
 20 25

<210> 183
 <211> 361
 <212> DNA
 <213> Conus lynceus

<400> 183
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctgc tagcggcctg tcaactacta 60
 cagcgtgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaactc 120
 tccatgctga ctcgggcctg ctggtcttcc ggaacacctt gtggtactga tagtttatgc 180
 tgcggtggat gcaatgtatc caaaagtaaa tgtaactagc tgattcggcg tctgaacttc 240
 ccccttctgt gctctatcct tttctgccc agtcctccat acctgagaat ggatcatgaac 300
 cactcatcac ctactcctct ggagacctca gaagagctac actgaaataa aagcgcattg 360
 c 361

<210> 184
 <211> 72
 <212> PRT
 <213> Conus lynceus

<400> 184
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Ala Ala
 1 5 10 15

Cys Gln Leu Leu His Ala Asp Asp Ser Arg Gly Thr Gln Lys Thr Ala
 20 25 30

Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp
 35 40 45

Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys
 50 55 60

Asn Val Ser Lys Ser Lys Cys Asn
 65 70

<210> 185
 <211> 27
 <212> PRT
 <213> Conus lynceus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 8 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp

<400> 185
 Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 186
 <211> 364
 <212> DNA
 <213> Conus lynceus

<400> 186
 atgaaactga cgtgtgtggt gatcgtcgcc gagctactcc taacggcctg tcaactcatc 60
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgac caccaatctc 120
 tccatgctga ctcggaagtg ctggtctccc ggaacctatt gtcgtgcgca tagtaaatgc 180
 tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc 240
 ctctttctgt gctctatcct ttttctgcct gagtctctcca tacctgagaa tggatcatgaa 300
 ccactcatca cctactcttc tggaggcctc agaggagcct aactgaaat aaaagccgca 360
 ttgg 364

<210> 187
 <211> 72
 <212> PRT
 <213> Conus lynceus

<400> 187
 Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45
 Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys
 50 55 60
 Asp Gln Asn Arg Asn Lys Cys Tyr
 65 70

<210> 188
 <211> 27
 <212> PRT
 <213> Conus lynceus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 5 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp; Xaa at residue 8 and 27 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 188
 Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys Cys
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa
 20 25

<210> 189
 <211> 318
 <212> DNA
 <213> Conus magus

<400> 189
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg gtacaggaaa accatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgtgg ctgatccagt 240
 gcctgatctt ccccttctg tgctctatcc ttttctgcc tgagtcctcc ttacctgaga 300
 gtggtcatga accactca 318

<210> 190
 <211> 71
 <212> PRT
 <213> Conus magus

<400> 190
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 191
 <211> 25
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 191
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 192
 <211> 259
 <212> DNA
 <213> Conus magus

<400> 192
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aagtcggaca ccaaactctc catgttaact ttgcgctgcy catcttacgg aaaaccttgt 180
 ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg 240
 atccggcgctc tgatcttcc 259

<210> 193
 <211> 72
 <212> PRT
 <213> Conus magus

<400> 193
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
 50 55 60
 Asp Pro Ala Arg Lys Thr Cys Thr
 65 70

<210> 194
 <211> 26
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 194
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 195

<211> 254
 <212> DNA
 <213> Conus magus

<400> 195
 gaatttttcag catcaccaaa accatcatca aaatgaaact gacgtgtgtg gtgatcgctg 60
 ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120
 agcatcgctgc cctgaggtcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag 180
 gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaata 240
 ttggctgata cgcc 254

<210> 196
 <211> 71
 <212> PRT
 <213> Conus magus

<400> 196
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60
 Cys Asn Arg Gly Lys Phe Gly
 65 70

<210> 197
 <211> 25
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 197
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 198
 <211> 358
 <212> DNA
 <213> Conus miles

<400> 198
 ggatccatga aactgacgtg cgtgggtgata atcgccatgc tgttcctgac agcctatcaa 60
 ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcggtgctct gaggccagct 120
 gacaaacacc tcagggttgac caagcggttg aatgatcgcg gtggagggttg cagtcaacat 180

cctcactgct gcggtggaac ttgcaataag cttattggcg tatgtctgta aagctgggtct 240
 gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcac catabctgtg 300
 aatgggtaag agccactcaa tacctattcc tctgggggct tcagaggaac tactttac 358

<210> 199
 <211> 74
 <212> PRT
 <213> Conus miles

<400> 199
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala
 1 5 10 15
 Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His
 20 25 30
 Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys
 35 40 45
 Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly
 50 55 60
 Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
 65 70

<210> 200
 <211> 27
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 12 is Pro or Hyp

<400> 200
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly
 1 5 10 15
 Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
 20 25

<210> 201
 <211> 292
 <212> DNA
 <213> Conus monachus

<400> 201
 accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaagtgtg ctgatccagc 240
 gcctgatctt ccccttctg tgccttatcc ttttctgcct gagtcctcct ta 292

<210> 202
 <211> 71
 <212> PRT
 <213> Conus monachus

<400> 202
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser
 35 40 45
 Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60
 Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 203
 <211> 25
 <212> PRT
 <213> Conus monachus
 <220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 203
 Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 204
 <211> 258
 <212> DNA
 <213> Conus monachus

<400> 204
 accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggtg cgcagaagca tcgtgccctg 120
 aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcattgtagt 180
 aggaccatgt ataactgctg caccggttct tgcaacagag gtaaattgtg ctgatccagc 240
 gcctgatctt ccccttc 258

<210> 205
 <211> 71
 <212> PRT
 <213> Conus monachus

<400> 205
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Lys Cys Gly
 65 70

<210> 206
 <211> 25
 <212> PRT
 <213> Conus monachus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 206
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 207
 <211> 258
 <212> DNA
 <213> Conus obscurus

<400> 207
 ctctctctct ctctgctgga caggctgcct ccctgcatga aaggcggatc gtcatgccgc 60
 ggtactacgg gagtctgttg cggtttttgc agtgatttcg gctataaatg tagggactat 120
 ccccaaaact gatcttcccc cttetgtgct ctatcctttt ctgtccgagt cctcctgacc 180
 tgagagtggg catgaaccac tcatcaccta cccctctggg gcttcacagg atctacattg 240
 aaataaaaagc cgcattgc 258

<210> 208
 <211> 39
 <212> PRT
 <213> Conus obscurus

<400> 208
 Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg
 1 5 10 15

Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
 20 25 30

Cys Arg Asp Tyr Pro Gln Asn
 35

<210> 209
 <211> 35
 <212> PRT
 <213> Conus obscurus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at

residue 27 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 209
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa
20 25 30
Xaa Gln Asn
35

<210> 210
<211> 259
<212> DNA
<213> Conus obscurus

<400> 210
ctctctctct ctctgctgga caggctcgact cgctgcttgc ctgacggaac gtcttgcctt 60
tttagtagga tcagatgctg cggctacttgc agttcaatct taaagtcattg tgtgagctga 120
tccagcgggt gatcttcttc cctctgtgct ccctcctttt ctgcttgagt tctccttacc 180
tgagagtggg catgaaccac tcatcaccta ctcttctgga ggcttcagag gagctacatt 240
gaaataaaag ccgcattgc 259

<210> 211
<211> 32
<212> PRT
<213> Conus obscurus

<400> 211
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
1 5 10 15

Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25 30

<210> 212
<211> 28
<212> PRT
<213> Conus monachus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 3 is Pro or Hyp

<400> 212
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210> 213
<211> 330
<212> DNA
<213> Conus pulicarius

<220>
<221> misc_feature
<222> (1)..(330)

<223> n may be any nucleotide

<400> 213
 atgaaactga cgtgtgtggt gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt 60
 acagctgaga cttactccag aggtaagcag aagcaccgtg ctttgaggtc aactgacaaa 120
 aactccaagt tgactaggca gtgctcgcc aacggtggat cttgttctcg tcattttcac 180
 tgctgcagcc tctattgcaa taaaaatact ggcgtatgta ttgcaaccta ataccctgtg 240
 gtgggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
 aaaactgcat tgcnttgacc aaaaaaaaaa 330

<210> 214
 <211> 76
 <212> PRT
 <213> Conus pulicarius

<400> 214
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His
 20 25 30
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
 35 40 45
 Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
 50 55 60
 Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
 65 70 75

<210> 215
 <211> 30
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 4 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 215
 Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
 20 25 30

<210> 216
 <211> 282
 <212> DNA
 <213> Conus purpurascens

<400> 216
 atgaaactga cgtgtgtggt gatcgctgcc gtgctgttcc tgacggcctg tcaactcatc 60
 acagctgatg actccagacg tacgcagaag catcgtgccc tgaggctcgac caccaaaggc 120

gccacgtcga atcgcccctg caagacaccc ggacgaaaat gttttccgca tcagaaggac 180
 tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240
 tccttttctg cctgagtctc cttacctgag agtgggtcatg aa 282

<210> 217
 <211> 72
 <212> PRT
 <213> Conus purpurascens

<400> 217
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys
 35 40 45
 Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
 50 55 60
 Ala Cys Ile Ile Thr Ile Cys Pro
 65 70

<210> 218
 <211> 27
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1, 5, 11 and 27 is Pro or Hyp

<400> 218
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
 1 5 10 15
 Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
 20 25

<210> 219
 <211> 340
 <212> DNA
 <213> Conus purpurascens

<400> 219
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccggagc atattgtaat 180
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240
 gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct tacctaagag 300
 tgggtcatgaa ccaactcatca ccttctcctc tggaggcttc 340

<210> 220
 <211> 71
 <212> PRT

<213> Conus purpurascens

<400> 220

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu
35 40 45

Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys
50 55 60

Lys Val Gly Gly Thr Cys Gly
65 70

<210> 221

<211> 26

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa
at residue 5 is Pro or Hyp; Xaa at residue 8 and 14
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 221

Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys
1 5 10 15

Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
20 25

<210> 222

<211> 317

<212> DNA

<213> Conus purpurascens

<400> 222

atgaaactga cgtgtgtggt gatcgctgcc gtgctgttcc tgacggcctg tcaactcatc 60

acagctgatg actccagacg tacgcagaag catcgtgcc tgaggctgac caccaaacgc 120

gccacgtcga atcgccctg caagaaaacc ggacgaaaat gttttccgca tcagaaggac 180

tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240

tccttttctg cctgagtcct ccttacctga gagtggatcat gaaccactca tcaccttctc 300

ctctggaggc ttcagag 317

<210> 223

<211> 72

<212> PRT

<213> Conus purpurascens

<400> 223

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
35 40 45
Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro
65 70

<210> 224
<211> 27
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 1, 11 and 27 is Pro or Hyp

<400> 224
Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
20 25

<210> 225
<211> 328
<212> DNA
<213> Conus radiatus

<400> 225
gctgatgcct gatcttcacg gttcttcctt gtctcctttg gcatcaccaa aaccatcatc 60
aaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcttgacggc ctgtcaactc 120
atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggggtc gatcagcagt 180
ctctttaagt cgaccgcgtca tggctgcaaa cccctcaaac gtcgttggtt caatgataaa 240
gaatgctgca gcaaattttg caattcagtc cgaaagcagt gtggataaat ggctaaaaaa 300
ctgaataaaa gccgcattgc aaaaaaaaa 328

<210> 226
<211> 74
<212> PRT
<213> Conus radiatus

<400> 226
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys
35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
50 55 60

Phe Cys Asn Ser Val Arg Lys Gln Cys Gly
65 70

<210> 227
<211> 28
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu;
Xaa at residue 5 is Pro or Hyp

<400> 227
His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
20 25

<210> 228
<211> 250
<212> DNA
<213> Conus radiatus

<400> 228
gaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 60
atcacagctg atgactccag aggtatgcag aaacatcatg ccctggggtc gatcagcagt 120
ctctttaagt cgaccgctcg tggctgcaaa cccctcaaac gtcgttggtt caatgataaa 180
gaatgctgca gcaaattttg caattcagtc cgaaaccagt gtggataaat ggctaaaaaac 240
tgaataaaag 250

<210> 229
<211> 74
<212> PRT
<213> Conus radiatus

<400> 229
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys
35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
50 55 60

Phe Cys Asn Ser Val Arg Asn Gln Cys Gly
65 70

<210> 230
<211> 28
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 15 is Glu or gamma-carboxy Glu;
Xaa at residue 5 is Pro or Hyp

<400> 230

Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
20 25

<210> 231

<211> 435

<212> DNA

<213> *Conus radiatus*

<400> 231

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ggaattccgc ttgcacggcg aacctgactt catctttctt cctgcctcc tttggcatca      60
ccaaaaccat catcaaatg aaactgacgt gtgtggtgat cgtcgccgtg ctggtcctga      120
cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga      180
ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgtagag      240
tttcttcgta taactgctgc tcttcttgca aatcatacaa caagaaatgt ggctgaactt      300
ccccttctgt gctctatcct ttctctgccc gagtctctcca tacctgagag tagtcatgaa      360
ccactgatta cctactcttc tggagggcct cagaggagct actttgaaat aaaagcccgc      420
attgcaaaaa aaaaaa                                     435

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<210> 232

<211> 72

<212> PRT

<213> *Conus radiatus*

<400> 232

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
20 25 30

Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro
35 40 45

Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys
50 55 60

Lys Ser Tyr Asn Lys Lys Cys Gly
65 70

<210> 233

<211> 27

<212> PRT

<213> *Conus radiatus*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at
residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,

di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 233

Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys
 1 5 10 15

Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly
 20 25

<210> 234

<211> 392

<212> DNA

<213> Conus rattus

<400> 234

ggatccatga aactgacgtg catggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120
 gacaaacaca tcagggttgac caagcgttgc aatgctcgca atgatggttg cagtcaacat 180
 tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctgggtct 240
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg 300
 aatgggttaag agccactcaa tacctactcc tctggggggt tcagaggaac tacattaaat 360
 aaagccacat tgcaaaaaaaaa aaaaaaaaaa aa 392

<210> 235

<211> 74

<212> PRT

<213> Conus rattus

<400> 235

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys
 35 40 45

Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly
 50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 65 70

<210> 236

<211> 27

<212> PRT

<213> Conus rattus

<400> 236

Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 237

<211> 395

<212> DNA
 <213> Conus rattus
 <400> 237
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
 ctcgatgcag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120
 gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180
 cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct 240
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac catacctgtg 300
 aatgggtaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360
 aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395

<210> 238
 <211> 74
 <212> PRT
 <213> Conus rattus

<400> 238
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30
 Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
 35 40 45
 Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
 50 55 60
 Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 65 70

<210> 239
 <211> 27
 <212> PRT
 <213> Conus rattus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 12 is Pro or Hyp

<400> 239
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 240
 <211> 390
 <212> DNA
 <213> Conus rattus

<400> 240
 ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120

gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtgggtg cagtcaacat 180
 cctcaatgct gcagtggatc ttgcaataag actttgggcg tatgtctgta aagctggtct 240
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac catacctgtg 300
 aatggttaag agccaactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360
 aaagccacat tgaaaaaaaa aaaaaaaaaa 390

<210> 241
 <211> 74
 <212> PRT
 <213> Conus rattus

<400> 241
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30
 Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
 35 40 45
 Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
 50 55 60
 Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 65 70

<210> 242
 <211> 27
 <212> PRT
 <213> Conus rattus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 12 is Pro or Hyp

<400> 242
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 20 25

<210> 243
 <211> 379
 <212> DNA
 <213> Conus stercusmuscarum

<400> 243
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180
 aggcttatgt atgactgctg cagcgggttct tgcagcggct acacaggtag atgtggctga 240
 tccagcgctt gatcttcccc cttctgtgct ctatcctttt ctgcctgggt cctccttacc 300
 tgagagtggg catgaaccac tcatcaccta ctctctgga ggctcagag gagttacaat 360

gaaataaaaag ccgcattgc

<210> 244
 <211> 73
 <212> PRT
 <213> Conus stercusmuscarum

<400> 244
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser
 35 40 45
 Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60
 Cys Ser Gly Tyr Thr Gly Arg Cys Gly
 65 70

<210> 245
 <211> 27
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 245
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys
 20 25

<210> 246
 <211> 35
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 246
 Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg
 1 5 10 15
 Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
 20 25 30
 Xaa Ser Asn
 35

<210> 247

<211> 380
 <212> DNA
 <213> Conus stercusmuscarum

<400> 247
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcgaaga ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180
 ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgtagctg 240
 atccggcgctc tgatcttccc ctttctgtgc tctatccttt tctgcctgag tcctccttac 300
 ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggcctcaga ggagctacaa 360
 tgaaataaaa gccgcattgc 380

<210> 248
 <211> 72
 <212> PRT
 <213> Conus stercusmuscarum

<400> 248
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
 50 55 60
 Asp Pro Ala Arg Asn Ile Cys Thr
 65 70

<210> 249
 <211> 26
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 249
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
 20 25

<210> 250
 <211> 388
 <212> DNA
 <213> Conus stercusmuscarum
 <400> 250
 ggatccatga aactgacgtg tgtggtgatt gtcgccgtgc tgctcctgac ggccctgtcaa 60

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ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcgaagacc 120
aaactctcca tgttaacttt gcgctgcgta tcttacggaa aaccttgtgg tattgacaac 180
gactgctgca atgcatgcga tccagccaga aatatatgta cgtagctgat ccggcgtctg 240
atcttcccc ttctgtgctc tacccttttc tgcttgggtc ctccttacct gagagtggtc 300
atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaagc 360
cgcattgcaa aaaaaaaaaa aaaaaaaaaa 388

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<210> 251
<211> 72
<212> PRT
<213> Conus stercusmuscarum

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<400> 251
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
          20          25          30
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val
          35          40          45
Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
          50          55          60
Asp Pro Ala Arg Asn Ile Cys Thr
65          70

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<210> 252
<211> 26
<212> PRT
<213> Conus stercusmuscarum

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<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
      residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
      di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 252
Cys Val Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
1          5          10          15
Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
          20          25

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<210> 253
<211> 264
<212> DNA
<213> Conus striatus

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<400> 253
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120
aggtcgacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga 180
cctactgtta tgaaaatctg ctgcggcttt tgcagtcgat acagcaaaat atgtatgaac 240

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tatccccaaaa attgatcttc cccc

264

<210> 254

<211> 78

<212> PRT

<213> Conus striatus

<400> 254

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn
65 70 75

<210> 255

<211> 36

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
residue 13, 25 and 34 is Pro or Hyp; Xaa at residue
10, 26 and 33 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 255

Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
20 25 30

Xaa Xaa Lys Asn
35

<210> 256

<211> 233

<212> DNA

<213> Conus striatus

<400> 256

gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60

cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc ccccttctg 120

tgctctatcc ttttctgcct gggtcctcct tacctgagag tggatcatgaa ccaactcatca 180

cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc 233

<210> 257

<211> 30

<212> PRT

<213> Conus striatus

<400> 257
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr
 1 5 10 15

Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly
 20 25 30

<210> 258
 <211> 26
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 258
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys
 1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
 20 25

<210> 259
 <211> 310
 <212> DNA
 <213> Conus striatus

<400> 259
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgcgg ctgatccagc 240
 gcctgatctt ccccttctg tgctctatcc tttctgctg agtcctctta cctgagagtg 300
 gtcatgaacc 310

<210> 260
 <211> 71
 <212> PRT
 <213> Conus striatus

<400> 260
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
 35 40 45

Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 261
 <211> 25
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 261
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 262
 <211> 256
 <212> DNA
 <213> Conus striatus

<400> 262
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt 180
 ggtatttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgtagctg 240
 atccggcgctc tgatct 256

<210> 263
 <211> 72
 <212> PRT
 <213> Conus striatus

<400> 263
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys
 50 55 60
 Asp Pro Ala Lys Lys Thr Cys Thr
 65 70

<210> 264
 <211> 26
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa

at residue 7 and 20 is Pro or Hyp; Xaa at residue 4
and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 264

Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr
20 25

<210> 265

<211> 229

<212> DNA

<213> Conus striatus

<400> 265

tctaggtcct cgggcagccc ctgtggtgtt actagtatat gctgtggtag atgctatagg 60

ggtaaagtga cgtagctcat cgggcgtctg atcttcccc ttctgtgtc catccttttc 120

tgcttgagtc ctctttacct gagagtggc gtgaaccact catcgctac tcctctggag 180

gcttcagagg ggctacacta aaataaaagc tatattgcaa tgaaaaaaa 229

<210> 266

<211> 24

<212> PRT

<213> Conus striatus

<400> 266

Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly
1 5 10 15

Arg Cys Tyr Arg Gly Lys Cys Thr
20

<210> 267

<211> 24

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 267

Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly
1 5 10 15

Arg Cys Xaa Arg Gly Lys Cys Thr
20

<210> 268

<211> 26

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,

di-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr

<400> 268

Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys
20 25

<210> 269

<211> 292

<212> DNA

<213> Conus striolatus

<400> 269

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgtctt gctgctcctg 60
acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120
aggctcgact ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt 180
aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc 240
gtctgatctt ccccttctg tgctctatcc ttttctgctt gagtctctct ta 292

<210> 270

<211> 71

<212> PRT

<213> Conus striolatus

<400> 270

Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Leu Thr Thr
1 5 10 15

Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser
50 55 60

Cys Asn Arg Gly Arg Cys Gly
65 70

<210> 271

<211> 25

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 271

Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 272

<211> 259
 <212> DNA
 <213> Conus striolatus

<400> 272
 accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgttgacg 60
 gcgtgtcaac tcatacacagc tgaggactcc agaggtacac agaagcatcg taccctgagg 120
 tcgaccgtca gacgctccaa gtccgagttg actacgagat gcaggccttc aggatccaac 180
 tgttgtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc 240
 gggcgtctga tctttcccc 259

<210> 273
 <211> 71
 <212> PRT
 <213> Conus striolatus

<400> 273
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys
 1 5 10 15
 Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr
 20 25 30
 Leu Arg Ser Thr Val Arg Arg Ser Lys Ser Glu Leu Thr Thr Arg Cys
 35 40 45
 Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly Arg
 50 55 60
 Cys Val Asn Arg Arg Cys Thr
 65 70

<210> 274
 <211> 24
 <212> PRT
 <213> Conus striolatus

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 3 is Pro or Hyp

<400> 274
 Cys Arg Xaa Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
 1 5 10 15
 Arg Cys Val Asn Arg Arg Cys Thr
 20

<210> 275
 <211> 280
 <212> DNA
 <213> Conus striolatus

<400> 275
 accaaaacca tcataaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgttcctg 60
 acggcgtgtc aactcatcac agctgaggac tccagaggta cacagaagca tcgttcacctg 120
 aggtcgacta ccaaagtctc caagtcgact agctgcatga aagccgggtc ttattgcgtc 180

gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattgactat 240
 cccaaaaact gatcttcccc ctactgtgct ctatcctttt 280

<210> 276
 <211> 77
 <212> PRT
 <213> Conus striolatus

<400> 276
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45
 Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
 50 55 60
 Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn
 65 70 75

<210> 277
 <211> 35
 <212> PRT
 <213> Conus striolatus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 277
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
 1 5 10 15
 Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa
 20 25 30

Xaa Lys Asn
 35

<210> 278
 <211> 174
 <212> DNA
 <213> Conus textile

<400> 278
 gttgactcgg tactgcacgc ctcatggagg acattgtggt tatkataatg actgctgcag 60
 tcatcaatgc aatataaaca gaaataaatg tgagtagctg atctggcatc tgatctgtgc 120
 tcgtccttac ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggc 174

<210> 279
 <211> 31
 <212> PRT
 <213> Conus textile

<400> 279

Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn
 1 5 10 15

Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25 30

<210> 280
 <211> 28
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 is Pro or Hyp; Xaa at residue 1 and 11
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 280
 Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 281
 <211> 28
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 is Pro or Hyp; Xaa at residue 1 and 11
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 281
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 282
 <211> 379
 <212> DNA
 <213> Conus tulipa

<400> 282
 accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcatcac agctctgcac tccagaggtg cgcagaagca tcgtgccctg 120
 gggcggacca ccaaactcac cttgtcgact cgctgcaaat caccggatc tccatgttca 180
 ccgactagtt ataattgctg ctggtcttgc agtccataca gaaaaaatg taggggctaa 240
 tccagcgcct gattttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300
 tgaaagtggg catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360
 gaaataaaag ccgcattgc 379

<210> 283
 <211> 73
 <212> PRT
 <213> Conus tulipa

<400> 283
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 35 40 45
 Pro Gly Ser Pro Cys Ser Pro Thr Ser Tyr Asn Cys Cys Trp Ser Cys
 50 55 60
 Ser Pro Tyr Arg Lys Lys Cys Arg Gly
 65 70

<210> 284
 <211> 27
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa
 at residue 17 is Trp or Bromo Trp; Xaa at residue
 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 284
 Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15
 Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg
 20 25

<210> 285
 <211> 379
 <212> DNA
 <213> Conus tulipa

<400> 285
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccttg 120
 gggtcgacca ccaaactcac cttgtcgact cgctgcttgt caccggatc ttcattgttca 180
 ccgactagtt ataattgctg caggtcttgc aatccatata gcagaaaatg taggggctaa 240
 tccagcgctt gatcttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300
 tgaaagtggg catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 286
 <211> 73
 <212> PRT
 <213> Conus tulipa

<400> 286
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser
 35 40 45
 Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 50 55 60
 Asn Pro Tyr Ser Arg Lys Cys Arg Gly
 65 70

<210> 287
 <211> 27
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 287
 Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15
 Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg
 20 25

<210> 288
 <211> 401
 <212> DNA
 <213> Conus viola

<400> 288
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag 180
 gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa 240
 gaatggtaaa tgtggctgat ccagcgcttg atcttcccc ttctgactgt ctccgacctt 300
 ttctgcctga gtcctcctta cctgagaggt gtcatgaacc actcatcacc tactcccctg 360
 gaagcttcag aggagctaca ttgaaataaa agccgcattg c 401

<210> 289
 <211> 76
 <212> PRT
 <213> Conus viola

<400> 289
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30
 Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr
 35 40 45
 Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys
 50 55 60
 Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
 65 70 75

<210> 290
 <211> 31
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 29 and 30 is Glu or gamma-carboxy
 Glu; Xaa at residue 11, 26 and 28 is Pro or Hyp;
 Xaa at residue 31 is Trp or Bromo-Trp

<400> 290
 Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa
 20 25 30

<210> 291
 <211> 372
 <212> DNA
 <213> Conus viola

<400> 291
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattat agctggggac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtagaggatc atcatgtcgt 180
 aggacttcgt atgactgctg cacgggttct tgcagaaatg gtaaattgtg ctgatccagc 240
 gcctgatctt ccccttctg tgcctcatcc ttttctgcct gagtcctcct tacctgagag 300
 tgggcatgaa ccaactcatca cctactccct ggaagcttca gaggagctac attgaaataa 360
 aagccgcatt gc 372

<210> 292
 <211> 71
 <212> PRT
 <213> Conus viola

<400> 292
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
 35 40 45

Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
50 55 60

Cys Arg Asn Gly Lys Cys Gly
65 70

<210> 293
<211> 25
<212> PRT
<213> Conus viola

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 293
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys
20 25

<210> 294
<211> 380
<212> DNA
<213> Conus viola

<400> 294
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
acggcctgtc agctcattac agctgaagac tccagaggta cgcagagca tcttgccctg 120
aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccagatc ttattgcgga 180
cctgctacta cgaaaatctg ctgcgatttt tgcagtcctat tcagcgatag atgtatgaac 240
aatcccaaca attgatcttc ccccttgtgt gctccatctt ttctgcctga gtcctcctta 300
cctgagagtg gtcatgaacc actcatcacc tactcctctg gaggcttcag aggagttaca 360
ttgaaataaa agccgcatgc 380

<210> 295
<211> 78
<212> PRT
<213> Conus viola

<400> 295
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
35 40 45

Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
65 70 75

<210> 296
 <211> 36
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa
 at residue 13, 25 and 34 is Pro or Hyp; Xaa at
 residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 296
 Ser Thr Ser Cys Met Xaa Ala Arg Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Xaa Asn Asn
 35

<210> 297
 <211> 373
 <212> DNA
 <213> Conus viola

<400> 297
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaggac tccagaggta cgcagttgca tcgtgccctg 120
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata 180
 aggattgcgt ataactgctg caagtattct tgcggaaatg gtaaattgtgg ctgatccagc 240
 gcctgatctt ccccttctgtg tgctccatcc ttttctgcc tgagtctctc ttacctgaga 300
 gtggtcatga accactcatc acctactcct ctggaggctt cagaggagct acattgaaat 360
 aaaagccgca tgc 373

<210> 298
 <211> 71
 <212> PRT
 <213> Conus viola

<400> 298
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30
 Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
 35 40 45
 Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
 50 55 60
 Cys Gly Asn Gly Lys Cys Gly
 65 70

<210> 299
 <211> 25
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 3 is Pro or Hyp; Xaa at residue
 13 and 18 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 299
 Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15
 Lys Xaa Ser Cys Gly Asn Gly Lys Cys
 20 25

<210> 300
 <211> 353
 <212> DNA
 <213> Conus viola

<400> 300
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg 60
 acggcctgtc aattcatcac agctgatgac tccagaagta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaaacactt tatgttgact tggtagtgca cgccttatgg aggacattgt 180
 ggttattata atgactgctg cagtcacaa tgcaatataa acagaaataa atgtgagtag 240
 ctgatccggc atctgatctg tgctcgccct aacctgagag tggatcatgaa ccaactcatca 300
 tctactcctc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 353

<210> 301
 <211> 73
 <212> PRT
 <213> Conus viola

<400> 301
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr
 35 40 45
 Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
 50 55 60
 Cys Asn Ile Asn Arg Asn Lys Cys Glu
 65 70

<210> 302
 <211> 28
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 302

Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa Xaa Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
20 25

<210> 303

<211> 294

<212> DNA

<213> Conus pulicarius

<400> 303

ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60
ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120
gacaaaaact ccaagttgac cagggaatgc acacctccag atggagcttg tggtttacct 180
acacactgct gcggggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240
tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 304

<211> 73

<212> PRT

<213> Conus pulicarius

<400> 304

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys
35 40 45

Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu
65 70

<210> 305

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu;
Xaa at residue 4, 5 and 12 is Pro or Hyp

<400> 305

Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 306
<211> 294
<212> DNA
<213> Conus pulicarius

<400> 306
ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60
ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120
gacaaaaact cccagttgac cagggaaatgc acacctccag gtggagcttg tggtttacct 180
acacactgct gcggggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240
tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 307
<211> 73
<212> PRT
<213> Conus pulicarius

<400> 307
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
20 25 30
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
35 40 45
Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
50 55 60
Cys Asp Met Ala Asn Asn Arg Cys Leu
65 70

<210> 308
<211> 27
<212> PRT
<213> Conus pulicarius

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa
at residue 4, 5 and 12 is Pro or Hyp

<400> 308
Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
1 5 10 15
Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 309
<211> 307
<212> DNA
<213> Conus rattus

<400> 309
ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa 60

cctgttataa ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact 120
gacggcaact cccggttgac cagggcatgc acgcctgaag gtggagcctg tagtagtggg 180
cgtcactgct gcggcttttg cgataacgtg tcccacacgt gctatgggtga aacaccatct 240
ctccactgat gtttccctt ctgtgctcta tcttcttttg cctgagtcac ccatacctgt 300
gctcgag 307

<210> 310
<211> 80
<212> PRT
<213> Conus rattus

<400> 310
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala
1 5 10 15
Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg
20 25 30
Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys
35 40 45
Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe
50 55 60
Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His
65 70 75 80

<210> 311
<211> 34
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residue 5 and 29 is Glu or gamma-carboxy
Glu; Xaa at residue 4 and 31 is Pro or Hyp; Xaa at
residue 27 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 311
Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
1 5 10 15
Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser
20 25 30

Leu His

<210> 312
<211> 342
<212> DNA
<213> Conus stercusmuscarum

<220>
<221> misc_feature
<222> (1)..(342)
<223> n may be any nucleotide

<400> 312

agatccatga aactgacgtg cgtggtgac gtcgccgtgc tgctcctgac ggccctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcggacacc 120
 aaactcccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat 180
 gactgctgca gcggttctctg caccagaggt agatgtggct gatccagcgc ctgatcttcc 240
 cccttctgtg ctctatcctt ttctgcctga gtcatcatac ctgtgctcga gcgttactag 300
 tggatccgag ctcggtacca agcttggcgt aatcataaaa nc 342

<210> 313
 <211> 71
 <212> PRT
 <213> Conus stercusmuscarum

<400> 313
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60
 Cys Thr Arg Gly Arg Cys Gly
 65 70

<210> 314
 <211> 25
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 314
 Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Xaa Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Thr Arg Gly Arg Cys
 20 25

<210> 315
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 315
 Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
 20 25 30

Pro

<210> 316
 <211> 28
 <212> PRT
 <213> Conus arenatus

<400> 316
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys
 1 5 10 15
 Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
 20 25

<210> 317
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 317
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
 20 25 30

Pro

<210> 318
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 318
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
 20 25 30

Pro

<210> 319
 <211> 27
 <212> PRT
 <213> Conus arenatus

<400> 319
 Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
 1 5 10 15
 Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
 20 25

<210> 320
 <211> 28
 <212> PRT
 <213> Conus arenatus

<400> 320
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys
 1 5 10 15
 Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
 20 25

<210> 321

<211> 30
 <212> PRT
 <213> Conus arenatus

<400> 321
 Gln Cys Ser Pro Ile Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
 1 5 10 15
 Ser Asn His Cys Ile Lys Pro Ile Gly Arg Cys Val Ala Thr
 20 25 30

<210> 322
 <211> 30
 <212> PRT
 <213> Conus arenatus

<400> 322
 Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
 1 5 10 15
 Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr
 20 25 30

<210> 323
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<400> 323
 Cys Lys Gly Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 324
 <211> 32
 <212> PRT
 <213> Conus aurisiacus

<400> 324
 Cys Met Glu Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys
 1 5 10 15
 Gly Phe Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
 20 25 30

<210> 325
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<400> 325
 Cys Lys Ala Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 326
 <211> 26
 <212> PRT
 <213> Conus aurisiacus

<400> 326
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr
 20 25

<210> 327
 <211> 36
 <212> PRT
 <213> Conus bullatus

<400> 327
 Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Pro Asn Asn
 35

<210> 328
 <211> 31
 <212> PRT
 <213> Conus bullatus

<400> 328
 Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
 1 5 10 15
 Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
 20 25 30

<210> 329
 <211> 26
 <212> PRT
 <213> Conus bullatus

<400> 329
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr
 20 25

<210> 330
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 330
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Lys Tyr Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 331
 <211> 36
 <212> PRT
 <213> Conus bullatus

<400> 331

Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys
20 25 30

Lys Pro Asn Asn
35

<210> 332
<211> 25
<212> PRT
<213> Conus bullatus

<400> 332
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys
20 25

<210> 333
<211> 25
<212> PRT
<213> Conus catus

<400> 333
Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys
20 25

<210> 334
<211> 25
<212> PRT
<213> Conus catus

<400> 334
Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys
20 25

<210> 335
<211> 28
<212> PRT
<213> Conus catus

<400> 335
Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
20 25

<210> 336
<211> 25
<212> PRT
<213> Conus catus

<400> 336
Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 337
<211> 26
<212> PRT
<213> Conus catus

<400> 337
Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25

<210> 338
<211> 25
<212> PRT
<213> Conus catus

<400> 338
Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 339
<211> 33
<212> PRT
<213> Conus characteristicus

<400> 339
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
20 25 30

Pro

<210> 340
<211> 26
<212> PRT
<213> Conus consors

<400> 340
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25

<210> 341
<211> 25
<212> PRT
<213> Conus consors

<400> 341
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys

20

25

<210> 342
 <211> 36
 <212> PRT
 <213> Conus consors

<400> 342
 Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
 1 5 10 15
 Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
 20 25 30
 Tyr Pro Gln Asn
 35

<210> 343
 <211> 27
 <212> PRT
 <213> Conus catus

<400> 343
 Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys
 1 5 10 15
 His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
 20 25

<210> 344
 <211> 25
 <212> PRT
 <213> Conus consors

<400> 344
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 345
 <211> 26
 <212> PRT
 <213> Conus consors

<400> 345
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 346
 <211> 25
 <212> PRT
 <213> Conus consors

<400> 346
 Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 347

<211> 35
 <212> PRT
 <213> Conus consors

<400> 347
 Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe
 20 25 30

Pro Ser Asn
 35

<210> 348
 <211> 25
 <212> PRT
 <213> Conus circumciscus

<400> 348
 Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Asn Gly Arg Cys
 20 25

<210> 349
 <211> 35
 <212> PRT
 <213> Conus circumciscus

<400> 349
 Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe
 20 25 30

Pro Ser Asn
 35

<210> 350
 <211> 27
 <212> PRT
 <213> Conus circumciscus

<400> 350
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys
 20 25

<210> 351
 <211> 35
 <212> PRT
 <213> Conus circumciscus

<400> 351
 Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
 20 25 30

Pro Ser Asn
35

<210> 352
<211> 28
<212> PRT
<213> Conus dalli

<400> 352
Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu
20 25

<210> 353
<211> 25
<212> PRT
<213> Conus distans

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa is Hyp

<400> 353
Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
20 25

<210> 354
<211> 27
<212> PRT
<213> Conus ermineus

<400> 354
Pro Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
1 5 10 15

Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro
20 25

<210> 355
<211> 27
<212> PRT
<213> Conus ermineus

<400> 355
Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
20 25

<210> 356
<211> 27
<212> PRT
<213> Conus geographus

<400> 356
Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys
1 5 10 15

Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr
20 25

<210> 357
<211> 29
<212> PRT
<213> Conus geographus

<400> 357
Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys
1 5 10 15

Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
20 25

<210> 358
<211> 30
<212> PRT
<213> Unknown

<220>
<223> unknown Conus species

<400> 358
Cys Leu Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
1 5 10 15

Thr Ser Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
20 25 30

<210> 359
<211> 27
<212> PRT
<213> Unknown

<220>
<223> unknown Conus species

<400> 359
Cys Lys Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys
1 5 10 15

Ser Lys Phe Cys Asn Glu His Leu His Met Cys
20 25

<210> 360
<211> 26
<212> PRT
<213> Unknown

<220>
<223> unknown Conus species

<400> 360
Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys
1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys
20 25

<210> 361
<211> 28
<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 361

Cys Ala Gly Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
20 25

<210> 362

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 362

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Tyr
20 25

<210> 363

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 363

Cys Leu Pro Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys
1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
20 25

<210> 364

<211> 30

<212> PRT

<213> Conus lynceus

<400> 364

Cys Lys Ser Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys
1 5 10 15

Thr Phe Cys Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
20 25 30

<210> 365

<211> 28

<212> PRT

<213> Conus lynceus

<400> 365

Cys Ala Gly Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
20 25

<210> 366

<211> 27

<212> PRT

<213> Conus lynceus

<400> 366

Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 367

<211> 27

<212> PRT

<213> *Conus lynceus*

<400> 367

Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr
 20 25

<210> 368

<211> 29

<212> PRT

<213> *Conus laterculatus*

<400> 368

Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
 20 25

<210> 369

<211> 27

<212> PRT

<213> *Conus laterculatus*

<400> 369

Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
 1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
 20 25

<210> 370

<211> 27

<212> PRT

<213> *Conus laterculatus*

<400> 370

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 371

<211> 37

<212> PRT

<213> *Conus leopardus*

<400> 371

Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys
 1 5 10 15

Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser
 20 25 30

Gly Pro Tyr Ser Ile
 35

<210> 372
 <211> 30
 <212> PRT
 <213> Conus leopardus

<400> 372
 Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro
 1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 373
 <211> 31
 <212> PRT
 <213> Conus leopardus

<400> 373
 Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu
 1 5 10 15

Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 20 25 30

<210> 374
 <211> 27
 <212> PRT
 <213> Conus leopardus

<400> 374
 Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 5 10 15

Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg
 20 25

<210> 375
 <211> 25
 <212> PRT
 <213> Conus magus

<400> 375
 Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 376
 <211> 26
 <212> PRT
 <213> Conus magus

<400> 376
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 377
 <211> 27
 <212> PRT
 <213> Conus miles

<400> 377
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly
 1 5 10 15
 Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
 20 25

<210> 378
 <211> 25
 <212> PRT
 <213> Conus monachus

<400> 378
 Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 379
 <211> 25
 <212> PRT
 <213> Conus monachus

<400> 379
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 380
 <211> 35
 <212> PRT
 <213> Conus obscurus

<400> 380
 Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
 1 5 10 15
 Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr
 20 25 30
 Pro Gln Asn
 35

<210> 381
 <211> 28
 <212> PRT
 <213> Conus obscurus

<400> 381
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15
 Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
 20 25

<210> 382

<211> 27
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa is Hyp

<400> 382
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
 20 25

<210> 383
 <211> 26
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

<400> 383
 Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys
 1 5 10 15
 Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
 20 25

<210> 384
 <211> 27
 <212> PRT
 <213> Conus purpurascens

<400> 384
 Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
 20 25

<210> 385
 <211> 30
 <212> PRT
 <213> Conus pulicarius

<400> 385
 Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
 20 25 30

<210> 386
 <211> 27
 <212> PRT
 <213> Conus pulicarius

<400> 386
 Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 387
<211> 27
<212> PRT
<213> Conus pulicarius

<400> 387
Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 388
<211> 28
<212> PRT
<213> Conus radiatus

<400> 388
His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
20 25

<210> 389
<211> 28
<212> PRT
<213> Conus radiatus

<400> 389
Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
20 25

<210> 390
<211> 27
<212> PRT
<213> Conus rattus

<400> 390
Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
20 25

<210> 391
<211> 27
<212> PRT
<213> Conus rattus

<400> 391
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
20 25

<210> 392

<211> 27
 <212> PRT
 <213> Conus rattus

<400> 392
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 20 25

<210> 393
 <211> 34
 <212> PRT
 <213> Conus rattus

<400> 393
 Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
 1 5 10 15
 Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser
 20 25 30

Leu His

<210> 394
 <211> 36
 <212> PRT
 <213> Conus striatus

<400> 394
 Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
 1 5 10 15
 Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
 20 25 30

Tyr Pro Lys Asn
 35

<210> 395
 <211> 26
 <212> PRT
 <213> Conus striatus

<400> 395
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
 20 25

<210> 396
 <211> 25
 <212> PRT
 <213> Conus striatus

<400> 396
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 397

<211> 26
 <212> PRT
 <213> Conus striatus

<400> 397
 Cys Glu Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr
 20 25

<210> 398
 <211> 27
 <212> PRT
 <213> Conus stercusmuscarum

<400> 398
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys
 20 25

<210> 399
 <211> 35
 <212> PRT
 <213> Conus stercusmuscarum
 <400> 399
 Thr Thr Ser Cys Met Gln Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg
 1 5 10 15
 Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
 20 25 30
 Pro Ser Asn
 35

<210> 400
 <211> 26
 <212> PRT
 <213> Conus stercusmuscarum

<400> 400
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
 20 25

<210> 401
 <211> 26
 <212> PRT
 <213> Conus stercusmuscarum

<400> 401
 Cys Val Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
 20 25

<210> 402
 <211> 25
 <212> PRT
 <213> Conus stercusmuscarum

<400> 402

Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys
 1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys
 20 25

<210> 403

<211> 25

<212> PRT

<213> Conus striolatus

<400> 403

Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 404

<211> 24

<212> PRT

<213> Conus striolatus

<400> 404

Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
 1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr
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<210> 405

<211> 35

<212> PRT

<213> Conus striolatus

<400> 405

Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg
 1 5 10 15

Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr
 20 25 30

Pro Lys Asn
 35

<210> 406

<211> 28

<212> PRT

<213> Conus textile

<400> 406

Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 407

<211> 31

<212> PRT

<213> Conus viola

<400> 407

113

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
 20 25 30

<210> 408
 <211> 25
 <212> PRT
 <213> Conus viola

<400> 408
 Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 409
 <211> 36
 <212> PRT
 <213> Conus viola

<400> 409
 Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Pro Asn Asn
 35

<210> 410
 <211> 25
 <212> PRT
 <213> Conus viola

<400> 410
 Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15

Lys Tyr Ser Cys Gly Asn Gly Lys Cys
 20 25

<210> 411
 <211> 28
 <212> PRT
 <213> Conus viola

<400> 411
 Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 412
 <211> 27
 <212> PRT
 <213> Conus textile

<400> 412

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser
 1 5 10 15

His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 413

<211> 26

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa is Hyp

<400> 413

Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys
 1 5 10 15

Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys
 20 25